

Appendix B

NCBI Entrez BLAST 2 sequences BLAST 2 sequences Example Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#).

Reference: Tatjana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program blastp Matrix Not Applicable

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use Mega BLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

[Browse](#)

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

LXXXXXXLXXXXVXXLKEXQALQTVCIL

[Browse](#)

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

[Browse](#)

A 1/3

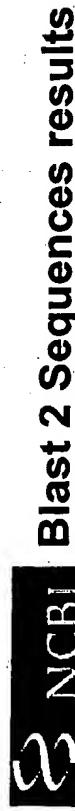
VASLRQQVEALQQVQHQLQAAFSQYKK
[ANON] [Clear input]
[ANON]

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

A 2/3

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>

11-06-2004



Blast 2 Sequences results

[PubMed](#) [Entrez](#) [BLAST](#) [OMIM](#) [Taxonomy](#) [Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix BLOSUM62 gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 lcl|seq_1 Length 26

Sequence 2 lcl|seq_2 Length 27

No significant similarity was found

A 3/3

NCBI Entrez BLAST BLAST 2 sequences Example Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCB1 ftp site.

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program blastp Matrix Not Applicable

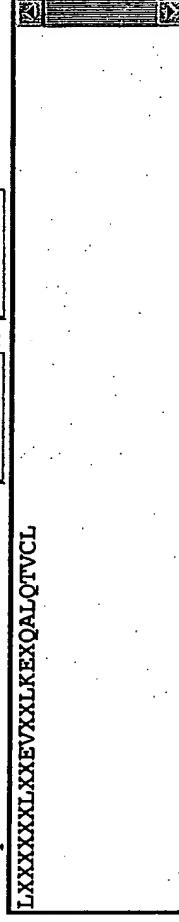
Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use MegaBLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

Sequence 1 Enter accession or GI or download from file
or sequence in FASTA format from: to:

LXXXXXXEVXXLKEXQALQTVCVCL


Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:





B 1/3

VNALRQRVGILEGGOLQNAFSQYKK
[Align] [Clear Input]

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

B2/3

NCBI Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix BLOSUM62 gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 lcl|seq_1 Length 26

Sequence 2 lcl|seq_2 Length 27

No significant similarity was found

B 3/3

NCBI Entrez BLAST 2 sequences BLAST Example Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program blastp Matrix Not Applicable

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use MegabLAST Strand option Both strands

Open gap 11 and extension gap 1 penalties
gap x_dropoff 50 expect 10.0 word size 3 Filter Align

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: 0 to: 0

LXXXXXXEVXXXLREXQALQTVCL

Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: 0 to: 0

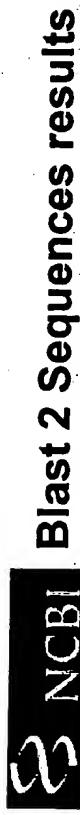
SAAIRQQMEALLNGKLQRLEAFSRYKK
<input type="checkbox"/> Align <input checked="" type="checkbox"/> Clear history

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

C 2/3

<http://www.ncbi.nlm.nih.gov/blast/b12seq/b12.html>

11-06-2004



Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix BLOSUM62 gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 lcl|seq_1 Length 26

Sequence 2 lcl|seq_2 Length 27

No significant similarity was found

C 3/3

[NCBI](#)[Entrez](#)[BLAST](#)[BLAST 2 sequences](#)[Help](#)

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBIs ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program blastp Matrix Not Applicable

Parameters used in BLASTN program only:

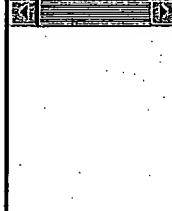
Reward for a match: Penalty for a mismatch:

Use Mega BLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

LXXXXXXVXXLKEEXQALQTVCL


Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

D 1/3

VNALKQRVTIILDGHILRRFQNQAFSQYKK
Align Clean Paste

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

D2/3

<http://www.ncbi.nlm.nih.gov/blast/b12seq/b12.html>

11-06-2004



Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix [BLOSUM62](#) gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0000 wordsize: 3 Filter Align

Sequence 1 lcl|seq_1 Length 26

Sequence 2 lcl|seq_2 Length 27

No significant similarity was found

D 3/3

[NCBI](#) [Entrez](#) [BLAST 2 sequences](#) [BLAST](#) [Example](#) [Help](#)

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program blastp Matrix Not Applicable

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use MegaBLAST Strand option Both strands

Open gap and extension gap penalties
gap x_dropoff expect word size Filter Align

Sequence 1 Enter accession or GI or download from file
or sequence in FASTA format from: to:



Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

E 113

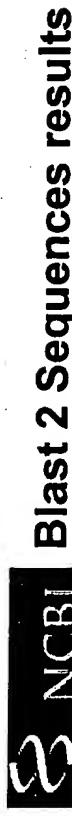
VDTLRORMRNLEGEVORLQNLIVTQYRK	
<input type="button" value="Align"/>	<input type="button" value="Create Input"/>

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

E 2/3

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>

11-06-2004



Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix BLOSUM62 gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 lcl|seq_1 Length 26

Sequence 2 lcl|seq_2 Length 27

No significant similarity was found

E 3/3